

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Polymeropoulos, Mihael  
Lavedan, Christian  
Leroy, Elisabeth  
Nussbaum, Robert  
Johnson, William  
Duvoisin, Roger
- (ii) TITLE OF INVENTION: Cloning of a gene mutation for  
Parkinson's disease
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SPENCER & FRANK
  - (B) STREET: 1100 New York Ave. Suite 300 East
  - (C) CITY: Washington
  - (D) STATE: D.C.
  - (E) COUNTRY: USA
  - (F) ZIP: 20005-3955
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 25-JUN-1998
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Schneller, John W.
  - (B) REGISTRATION NUMBER: 26,031
  - (C) REFERENCE/DOCKET NUMBER: NIH 0082A
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (202)414-4000
  - (B) TELEFAX: (202)414-4040

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 216 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: alpha synuclein gene/ exon 4 region

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTAATCAGC AATTTAAGGC TAGCTTGAGA CTTATGTCTT GAATTGTTT TTGTAGGCTC	60
CAAAACCAAG GAGGGAGTGG TGCATGCTGT GACAACAGGT AAGCTCCATT GTGCTTATAT	120
CAAAGATGAT ATNTAAAGTAT CTAGTGATTA GTGTGGCCCA GTATCAAGAT TCCTATGAA	181
ATTGTAAAACA ATCACTGAGC ATCTAAGAAC ATATC	216

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer #3"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCTAATCAGC AATTTAGGCT AG	22
--------------------------	----

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer #13"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTATACAAGA ATCTACGAGT C

21

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Swiss-Prot P37840

(vii) IMMEDIATE SOURCE:

- (B) CLONE: alpha synuclein protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val  
1                      5                      10                      15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys  
20                      25                      30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val  
35                      40                      45

Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr  
50                      55                      60

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys  
65                      70                      75                      80

Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys  
85                      90                      95

Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile  
100                      105                      110

Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro

115

120

125

Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala  
 130 135 140

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus norvegicus
- (C) INDIVIDUAL ISOLATE: Swiss-Prot P37377

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: alpha synuclein protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val  
 1 5 10 15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys  
 20 25 30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val  
 35 40 45

Val His Gly Val Thr Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr  
 50 55 60

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys  
 65 70 75 80

Thr Val Glu Gly Ala Gly Asn Ile Ala Ala Ala Thr Gly Phe Val Lys  
 85 90 95

Lys Asp Gln Met Gly Lys Gly Glu Glu Gly Tyr Pro Gln Glu Gly Ile  
 100 105 110

Leu Glu Asp Met Pro Val Asp Pro Ser Ser Glu Ala Tyr Glu Met Pro  
 115 120 125

Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala

130

135

140

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 134 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Bos taurus  
 (C) INDIVIDUAL ISOLATE: Swiss-Prot P33567
- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: alpha synuclein protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Phe	Met	Lys	Gly	Leu	Ser	Met	Ala	Lys	Glu	Gly	Val	Val	15
1				5				10								
Ala	Ala	Ala	Glu	Lys	Thr	Lys	Gln	Gly	Val	Thr	Glu	Ala	Ala	Glu	Lys	30
			20				25									
Thr	Lys	Glu	Gly	Val	Leu	Tyr	Val	Gly	Ser	Lys	Thr	Lys	Glu	Gly	Val	45
			35				40									
Val	Gln	Gly	Val	Ala	Ser	Val	Ala	Glu	Lys	Thr	Lys	Glu	Gln	Ala	Ser	60
			50				55									
His	Leu	Gly	Gly	Ala	Val	Phe	Ser	Gly	Ala	Gly	Asn	Ile	Ala	Ala	Ala	80
			65				70				75					
Thr	Gly	Leu	Val	Lys	Lys	Glu	Glu	Phe	Pro	Thr	Asp	Leu	Lys	Pro	Glu	95
				85				90								
Glu	Val	Ala	Gln	Glu	Ala	Ala	Glu	Glu	Pro	Leu	Ile	Glu	Pro	Leu	Met	110
			100				105									
Glu	Pro	Glu	Gly	Glu	Ser	Tyr	Glu	Glu	Gln	Pro	Gln	Glu	Glu	Tyr	Gln	125
			115				120									
Glu	Tyr	Glu	Pro	Glu	Ala											
				130												

## (2) INFORMATION FOR SEQ ID NO:7:



- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Torpedo californica
- (C) INDIVIDUAL ISOLATE: Swiss-Prot P37379

(vii) IMMEDIATE SOURCE:

- (B) CLONE: alpha synuclein homologue

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asp	Val	Leu	Lys	Lys	Gly	Phe	Ser	Phe	Ala	Lys	Glu	Gly	Val	Val	15
1				5					10							
Ala	Ala	Ala	Glu	Lys	Thr	Lys	Gln	Gly	Val	Gln	Asp	Ala	Ala	Glu	Lys	30
			20				25									
Thr	Lys	Gln	Gly	Val	Gln	Asp	Ala	Ala	Glu	Lys	Thr	Lys	Glu	Gly	Val	45
			35				40									
Met	Tyr	Val	Gly	Thr	Lys	Thr	Lys	Glu	Gly	Val	Val	Gln	Ser	Val	Asn	60
			50				55									
Thr	Val	Thr	Glu	Lys	Thr	Lys	Glu	Gln	Ala	Asn	Val	Val	Gly	Gly	Ala	80
			65			70			75							
Val	Val	Ala	Gly	Val	Asn	Thr	Val	Ala	Ser	Lys	Thr	Val	Glu	Gly	Val	95
				85				90								
Glu	Asn	Val	Ala	Ala	Ala	Ser	Gly	Val	Val	Lys	Leu	Asp	Glu	His	Gly	110
			100					105								
Arg	Glu	Ile	Pro	Ala	Glu	Gln	Val	Ala	Glu	Gly	Lys	Gln	Thr	Thr	Gln	125
			115				120									
Glu	Pro	Leu	Val	Glu	Ala	Thr	Glu	Ala	Thr	Glu	Glu	Thr	Gly	Lys		140
			130				135									

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer #1F"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGACAGTGT GTGTAAAGG

19

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer #13R"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
AACATCTGTC AGCAGATCTC

20

(2) INFORMATION FOR SEQ ID NO:11

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 2809 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) IMMEDIATE SOURCE:

(A) CLONE: BAC clone 139A20 HUMAN BETA SYNULEIN GENE

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGCCGCAGC CGCCGCTCCA TCCCCAGCCC CGGCCCCGCA TCCGGTTTGG AAGGGGGCTG  
CAAGTTTGCA AGGGGCCCCG GANAAAAANC GAGCAGTGGC CCTTCCCGCG TCCCCAGGGT  
TTCAAGGGAC GCTAGGANTN TCCGCGGCCC TGGAGGTTCTG CACTGGGGAG TGGGGTGAGA  
TGGGGGGAAA GCGGGAGGGG GCTCAGGGTC CAGAAGGGCN CCGCGGTCTC GGGAGTAGGG  
GGGCATNTGC GTCCCGCGG AGGGGCTGGG GTGAGAGTGC GGGGCCAGTG CACCGGTGCC  
CGTGTATCGC CCTCCCCAGG CCGCCAGGAT GGACGTGTTC ATGAAGGGCC TGTCCATGGC  
CAAGGAGGGC GTTGTGGCAG CCGCGGAGAA AACCAAGCAG GGGGTCACCG AGGCGGCGGA  
GAAGACCAAG GAGGGCGTCC TCTACGTCGG TGGGCNGGGG GCNNGGTTTC TGGGGCTGCA  
GGGCTGGGGG TCCCCCTACA GTGTGGAGCT GGGGCCGGGT CCCGGGGAGG GGGGTTCTGG  
GCAAGATAAT ATNANTCAGC AGATGGGGCN AGGTCANCAN GGGTCATAAG GGACATACCC  
ANCCCATAGA ANCCTGGGTC TGTATCCGGA AATGGGGACA CGGGGCGGGC TGATGAGGTG  
GGGGGCTCCA NCTGAAAGGC CAGGGACCAN TGCANTNATA AAANCACACA NCCTCCTTTT  
TCTTATCTTT TTTACCATTA TTAATAGTTA TCTGGTGTG AACACTTTCT GTATGCCAAG  
TACTGGGTAA AATGTCATAA CATCCATTTC CTCATGTAAT GCTTCCGCCC ATTCTACAGG  
TAAGGGAAAC TGGGCTTCCC ATTGGTAGNT AAATTTTAGG TTCAGAAAGG CTTGAATTGA  
ATGTCAGTTC AGCCAATTTC TTAGTGGTGG AACCAAAGTG AGTTCCATCC GTGAAACGGG  
GACAATAACA GCACCCGCTT CCCAGGGCTG GGGAAAAGTG AAGTGCAGCG GGGCAGGCAG  
AGGACTTGAC ACAGCACTGG CCCTCAGCCA ACATCCACTA GAGGGGTGGG GTATCGCATC  
AGGTGGGAGA GAACTGCAAC CCTTGCAGAC AGAGGTGTGG GGGCCAGTGC AGTGATAAGA  
CGGGGGTTAA CATGGGGGTG CAGGTTGTAG GATNTGGGGA CCCAAGGAGG CAGTGACGGG  
GCCAGGATGC CCACTCTGTA ATCACCATGC TGTGCTGGAG TTTCTGTTCC CTCAGCGCAG  
AGTCCTTAAA TGTGCCGCTT TTTCTNCCCT GCAGGAAGCA AGACCCGAGA AGGTGTGGTA  
CAAGGTGTGG CTTCAGGTAC TAGCCCAGCC CTGGCACCAG CCCTTCTCTC AMTTAGGCGG  
ATGATCTGGC CGGGAACCAG AGGGCGGGGG CGGGGGAGAC TCCCAAGGCT TCTGCGGGAA  
TGCTCCGTGG GGAGGGCAGG CCCTGGGATA CTACAAGGCA GGGCATCGGT GTTTCCCCCT  
GGCTCCCAAA CCCCTTCCTC AACCCCTCC CTGCTCCAGT GGCTGAAAAA ACCAAGGAAC

AGGCCTCACA TCTGGGAGGA GCTGTGTTCT CTGGGGCAGG GAACATCGCA GCAGCCACAG  
 GACTGGTGAA GAGGGAGGAA TTCCCTACTG ATCTGAAGGT AAGCGATCCT TCTGACCCGC  
 ACATGCAGGC AAACACACAC ACACACACAC ACACACACCN GGCACACAAA TAAACCTGTC  
 ACCATCCCCG CCCCCCTAAT CCTGCCACCA GCTTGGAACA CAAGCCACTT TGCCTCCCAT  
 CCTGCNGGCC CGTGCTAGAC TCAGCTCAGA ATGCATCTGA ATAANGGCGT GCATGGGTGT  
 GACGCTCCCC GTGATGGGGA CCCAGACCTG GCTGTCTGCG TGTATCCTGC TTGCCAGCGT  
 GACCCATATG ACTTCTGGCC ACGTCTGCAT GTGTCAATGA TTGTTCAATC ATTTCTTTTC  
 ATTCAACAAA TATCCATGCC ANANCCAGCC CTGTCCTTGA GCTTCCAGNT CCCTTTTCAGC  
 CNAGGGGAGC NTGAGGGTTA TTTTGGGGT CCCGATGCCC AGCACAGAGC CTGACACAAA  
 GGATGAGGCA TAAGCTGGTG ANTGAGTATC CAAATGGTGG AAGTGTGGAG GNTGCCAGGC  
 ATTGGGGGAG CGGCGTGGAG AGCCAGCTCC CCAATCCATG CTGCCACTTC AACTGTGATT  
 CGGGGGAATT TCCCCCTTCA CCTCCATCCC ACTTCCAAGG CACTCCAAAT AAATAACTGA  
 ATTAGAAATT ATCCTTGTTT TGCCAACCCA CCCTAGCCTT CCCCCTCCA ACCCACCCAA  
 AGCTTACCAC TGTGGGAATT TGGGGGGCAT CCTGGCTGTC CTCACGAGTC CTGACCTTTT  
 CTGCCCACAG CCAGAGGAAG TGGCCCAGGA AGCTGCTGAA GAACCACTGA TTGAGCCCCT  
 GATGGAGCCA GAAGGGGAGA GTTATGAGGA CCCACCCCAG GAGGAATATC AGGAGTATGA  
 GCCAGAGGCG TAGGGGCCCA GGAGAGCCCC CACCAGCAGC ACAATTCTGT CCCTGTCCCT  
 GCCCCGCCCC CCAGAGCCAG GGCTGTCCTT AGACTCCTTC TCCCCAATCA CGAGATCTTC  
 CTTCCGCTCT GAGGCAACCC CCTCGGAGCC TGTGTTAGTG TCTGTCCATC TGTCTGTCCT  
 ACCCGCCCGC GTCCAACCCC GGGGCATGGA CAGGGCCAGG GTTGCGGTG CGGCTGGGAG  
 CCTCGCCCCT CCAGTGTGTC CTCTCCCAT CCAGCGTCTG CGCG

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 223 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) IMMEDIATE SOURCE:

(A) CLONE: BAC clone 174P13 HUMAN GAMMA SYNULEIN GENE, 5' END

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGGGAGATCC AGCTCCGTCC TGCCTGCAGC AGCACAACCC TGCACACCCA CCATGGATGT  
CTTCAAGAAG GGCTTCTCCA TCGCCAAGGA GGGNGTGGTG GGTGCGGTGG AAAAGACCAA  
GCAGGGGGTG ACGGAAGCAG CTGAGAAGAC CAAGGAGGGG GTCATGTATG TGGGATTACA  
TTTTTTTTTT AAAGAAAGAA TAAATTAATT GTGATTAAAG TTG

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 677

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) IMMEDIATE SOURCE:

(A) CLONE: BAC clone 174P13 HUMAN GAMMA SYNULEIN GENE, 3' END

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTTTTTNAGG GGGGAAAACA GGGAATANAA AAANANGGGG GGGGGTTTTT NNGGGGGGGG  
GGGGAAAANG GTTNGGGGGN NAACCNAAAN AAANNCCNAN GGGGGGGGNN ANTNAANTTT  
TGGAACCCA AAGCCCNAGG AGGATTTTTN GTNAANAACG TNACCTCNAG TGGGNCGAGG

AAGACCAAGG AAANGCCCAA CNCGGTTGAN CGAGGCTGTG GTGAACANCG TNCAACNCTG  
TGCCCNCCAA NANC GTGGAG GNGGCGGAGA ACATCSCGGT CACCTCCGGG GTGGTGCGCM  
AGGAGGACTT GAGGCCATCT KCCCCCMAC AGGAGGGTGT GGCATCCMAA GARAAAGAGG  
AAGTGGCAGA GGAGGCCAG AGTGGGGGAR ACTAGAGGGC TACAGGCCAG CGTGGATGAC  
CTGAAGAGCG CTCCTCTGCC TTGGACACCA TCCCCTCCTA GCACAAGGAG TGCCCGCCTT  
GAGTGACATG CGGCTGCCCA CGCTCCTGCC CTCGTCTTCC TGGCCACCCT TGGCCTGTCC  
ACCTGTGCTG CTGCACCAAC CTCACTGCCC TCCCTCGGCC CCACCCACCC TCTGGTCCTT  
CTGACCCAC TTATGCTGCT GTGAATTTTT TTTTAAATG ATTCAAATA AACTTGAGC  
CCACTCCAAA AAAAAAA

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1181 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exons 1 and 2 plus  
flanking intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATTTTCAGCG ATGCGAGGGC AAAGCGCTCT CGGCGGTGCG GTGTGAGCCA CCTCCCGGCG  
 CTGCCTGTCT CCTCCAGCAG CTCCCAAGG GATAGGCTCT GCCCTTGGTG GTCGACCCCTC  
 AGGCCCTCGN TCTCCCAGGN CGACTCTGAC GAGGGGTAGG GGGTGGTCCC CNGGAGGACC  
 CAGAGGAAAG GCNNGGACAA GAAGGGAGGG GAAGGGGAAA GAGGAAGAGG CATCATCCCT  
 AGCCCAACCG CTCCCAGTCT CCACAAGAGT GCTCGTGACC CTAAACTTAA CGTGAGGCGC  
 AAAAGCGCCC CAACCTTTTC CCGCCTTGNN CCAGGCAGGC GGCTGGAGTT GATGGCTCAC  
 CCCGCGCCCC CTGCCCCATC CCCATCCGAG ATAGGGACGA GGAGCACGCT GCAGGGAAAG  
 CAGCGAGCGC CGGGAGAGGG GCGGGCAGAA GCGCTGACAA ATCAGCGGTG GGGGCGGAGA  
 GCCGAGGAGA AGGAGAAGGA GGAGGACTAG GAGGAGGAGG ACGGCGACGA CCAGAAGGGG  
 CCCAAGAGAG GGGGCGAGCG ACCGAGCGCC GCGACGCGAA GTGAGGTGCG TGCGGGCTCA  
 GCGCAGACCC CGGCCCGGCC CCTCCTGAGA GCGTCCTGGG CGCTCCCTCA CGCCTTGCTT  
 TCAAGCCTTC TGCCTTTCCA CCCTCGTGAG CGGAGAACTG GGAGTGGCCA TTCGACGACA  
 GGTTAGCGGG TTTGCCTCCC ACTCCCCCAG CCTCGCGTCG CCGGCTCACA GCGGCCTCCT  
 CTGGGGACAG TCCCCCCCCG GTGCCCCCTC GCCCTTCCTG TGCCTCCTT TTCCTTCTT  
 TTTCTATTA AATATTATTT GGGAATTGTT TAAATTTTTT TTTTAAAAAA AGAGAGAGGC  
 GNGGAGGAGT CGGAGTTGTG GAGAAGCAGA GGGACTCAGG TAAGTACCTG TGGATCTAAA  
 CGGGNGTCTT TTGGAAATCC TGGAGAACGC CGGATGGAGA CGAATGGTCG TGGGNACCGG  
 GAGGGGGTGG TGCTGCCATG AGGACCGCTG GGCCAGGTCT CTGGGAGGTG AGTACTTGTC  
 CTTTGGGGAG CTAAGGAAAG AGACTTGACC TGGCTTTCGT CCTGCTTCTG ATATTCCCTT  
 CTCCACAAGG GCTGAGAGNT TAGGCTGCTT CTCCGGGATC C

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 536 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 3 plus flanking  
intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTTAAAAGAG TCTCACACTT TGGAGGGTTT CTCATGATTT TTCAGTGTTT TTTGTTTATT  
TTTCCCCGAA AGTTCTCATT CAAAGTGTAT TTTATGTTTT CCAGTGTTGGT GTAAAGAAAT  
TCATTAGCCA TGGATGTATT CATGAAAGGA CTTTCAAAGG CCAAGGAGGG AGTTGTGGCT  
GCTGCTGAGA AAACCAAACA GGGTGTGGCA GAAGCAGCAG GAAAGACAAA AGAGGGTGTT  
CTCTATGTAG GTAGGTAAAC CCCAAATGTC AGTTTGGTGC TTGTTTCATGA GTGATGGGTT  
AGGATAACAA TACTCTAAAT GCTGGTAGTT CTCTCTCTTG ATTCATTTTT GCATCATTGC  
TTGTCAAAAA GGTGGACTGA GTCAGAGGTA TGTGTAGGTA GGTGAATGTG AACGTGTGTA  
TNTGAGCTAA TAGTAAAAAT GCGACTGTTT GCTTTTCAGA TTTTAAATTT TGCCTAATAT  
NTATGACTTN TTAAAATGAA TGTCTCTGTA CTACATAATT CTATNTCAGA GACAGT

(2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 650 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 4 plus flanking  
intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGCAGGTCA ACGGATCTGT CTCTAGTGCT GTACTTTTAA AGCTTCTACA GTTCTGAATT  
CAAAATTATC TTCTCACTGG GCCCCGGTGT TATCTCATTC TTTTCTCTCC TCTGTAAGTT  
GACATGTGAT GTGGGAACAA AGGGGATAAA GTCATTATTT TGTGCTAAAA TCGTAATTGG  
AGAGGACCTC CTGTTAGCTG GGCTTTCTTC TATNTATTGT GGTGGTTAGG AGTCCTTCT  
TCTAGTTTTA GGATATATAT ATATATTTTT TCTTCCCTG AAGATATAAT AATATATATA  
CTTCTGAAGA TTGAGATTTT TAAATTAGTT GTATTGAAAA CTAGCTAATC AGCAATTTAA  
GGCTAGCTTG AGACTTATGT CTTGAATTTG TTTTGTAGG CTCCAAAACC AAGGAGGGAG  
TGGTGCATGG TGTGGCAACA GGTAAGCTCC ATTGTGCTTA TATCAAAGAT GATATNTAAA  
GTATCTAGTG ATTAGTGTGG CCCAGTATCA AGATTCCTAT TGAAATTGTA AAACAATCAC  
TGAGCATCTA AGAACATATC AGTCTTATTG AACTGAATT CTTTATAAAG TATTTTTTAA  
TAGGTAAATA TTGATTATAA ATAAAAATA TACTTGCCAA GAATAATGAG

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 504 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR



(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 5 plus flanking  
intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATATCTTAGC CAAGATTCAA TGTTTGTTG AACCACACTC ACTTGACATC TTGGTGGCTT  
TTGTTTCTTC TGACCACTCA GTTATCTATG GCATGTGTAG ATACAGGTGT ATGGAANCGA  
TGGCTAGTGG AAGTGAATG ATTTTAAGTC ACTGTTATTC TACCACCCTT TAATCTGTTG  
TTGCTCTTTA TTTGTACCAG TGGCTGAGAA GACCAAAGAG CAAGTGACAA ATGTTGGAGG  
AGCAGTGGTG ACGGGTGTGA CAGCAGTAGC CCAGAAGACA GTGGAGGGAG CAGGGAGCAT  
TGCAGCAGCC ACTGGCTTTG TCAAAAAGGA CCAGTTGGGC AAGGTATGGC TGTGTACGTT  
TTGTGTTACA TTTATAAGCT GGTGAGATTA CGGTCATTT TCATGTGAAG CCTGGAGGCA  
GGAGCAAGAT ACTTACTGTG GGGAACGGCT ACCTGACCCT CCCCTTGTGA AAAAGTGCTA  
CCTTTATATT GGTCTTGCTT GTTT

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 727 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exons 1 and 2 plus  
flanking intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAAAGTTTAC ATACTTTGAG GTTGATAACC CATGTTGCCG CAATGTTTCC CCGGAGGCAT  
TGTGGAGTTT AGAATGCCAG TAGTAATATT AAGGTGTGCC ATTTTCAAGA TCCGTGGCCA  
ACATCCCTAT ATGTAAGATT TTTCCAAAAC ATGGTTCTGA TTTTAAAAG TGAAAAATGC  
TACTTCATCA TGTTCTTTTT GTGCTTCTTA CTTTAAATAT TAGAATGAAG AAGGAGCCCC  
ACAGGAAGGA ATTCTGGAAG ATATGCCTGT GGATCCTGAC AATGAGGCTT ATGAAATGCC  
TTCTGAGGTA GGAGTCCAAG CTGAATCTTT CTAACAAGAC AGTACCAAAA ACCTGTCATT  
GTCACATTTT TCTTTCATTA GTGCTTAGTG AGAATCATTT GCTCTCTACA TGCTCATTA  
GTGGACAAC TGAAGTTAA GAATAGTTTT TACATTTTAA AAGGGTCCTT AAAAAAAAAAG  
AGGAGGAGGA AGATGAAGAA GAGGAAGAAA GGATGTAAAA GAAATCATAT GTAGTCCACA  
TAGCTTAATA TACNTACTAC TTGACCCTTT ACAGGAAAAG CTTTACTAAC CCCTGCATTA  
GAGAATATAT TTTTTTGCAA AAACATTGAT TGTAATTTT AGTGTAAGT GGGGAGCCAT  
TTCCTATCTC ATTGGCTGTC CAGTGCTGAT GCGTAATTGA AACTTATACT AACAGTGTGT  
GCTGTCT

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1596 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 7 plus flanking  
intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTTGTATTTT TCTAATATTA GGAAGGGTAT CAAGACTACG AACCTGAAGC CTAAGAAATA  
TCTTTGCTCC CAGTTTCTTG AGATCTGCTG ACAGATGTTC CATCCTGTAC AAGTGCTCAG  
TTCCAATGTG CCCAGTCATG ACATTTCTCA AAGTTTTTAC AGTGTATCTC GAAGTCTTCC  
ATCAGCAGTG ATTGAAGCAT CTGTACCTGC CCCCCTCAG CATTCGGTG CTTCCTTTC  
ACTGAAGTGA ATACATGGTA GCAGGGTCTT TGTGTGCTGT GGATTTTGTG GCTTCAATCT  
ACGATGTTAA AACAAATTAA AAACACCTAA GTGACTACCA CTTATTTCTA AATCCTCACT  
ATTTTTTTGT TGCTGTTGTT CAGAAGTTGT TAGTGATTTG CTATCATATA TTATNAGATT  
TTTAGGTGTC TTTTAATGAT ACTGTCTAAG AATAATGACG TATTGTGAAA TTTGTTAATA  
TATATNATAC TTAAAAATAT GTGAGCATGA AACTATGCAC CTATAATACT AAATATGAAA  
TTTTACCATT TTGCGATGTG TTTTATTCAC TTGTGTTTGT ATATNAATGG TGAGAATTAA  
AATAAAACGT TATCTCATTG CAAAAATATT TTATTTTTAT CCCATCTCAC TTTAATAATA  
AAAATCATGC TTATAAGCAA CATGAATTAA GAACTGACAC AAAGGACAAA AATATAAAGT  
TATTAATAGC CATTTGAAGA AGGAGGAATT TTAGAAGAGG TAGAGAAAAT GGAACATTAA  
CCCTACACTC GGAATTCCCT GAAGCAACAC TGCCAGAAGT GTGTTTTGGT ATGCACTGGT  
TCCTTAAGTG GCTGTGATTA ATTATTGAAA GTGGGGTGTT GAAGACCCCA ACTACTATTG

TAGAGTGGTC TATTTCTCCC TTCAATCCTG TCAATGTTTG CTTTACGTAT TTTGGGGAAC  
TGTGTTTGA TGTGTATGTG TTTATAATTG TTATACATTT TTAATTGAGC CTTTTATTAA  
CATATATTGT TATTTTTGTC TCGAAATAAT TTTTAGTTA AAATCTATTT TGTCTGATAT  
TGGTGTGAAT GCTGTACCTT TCTGACAATA AATAATATNC GACCATGAAT AAAAAAAAAA  
AAAAAGTGGG TTCCCGGGAA CTAAGCAGTG TAGAAGATGA TTTTGACTAC ACCCTCCTTA  
GAGAGCCATA AGACACATTA GCACATATTA GCACATTCAA GGCTCTGAGA GAATGTGGTT  
AACTTTGTTT AACTCAGCAT TCCTCACTTT TTTTTTTTAA TCATCAGAAA TTCTCTCTCT  
CTCTCTCTTT TTCTCTCGCT CTCTTTTTTT TTTTTTTTTT TTTTACAGGA AATGCCTTTA  
AACATCGTTG GGAAC TACCA GAGTCACCTT AAAGGGAGNA TCAATTCTCT AGGACTGGAT  
AAAAATTTC TGGGCCTCCT TTAAAATGTT GCCCAAATAT ATGGAATTCT AGGGGTTTTT  
CCNTAGGGGG AAGGGTTTTT TCTCTTTTCN GGGGAGGATC CTTTTAACNC CCCNGGGGGG  
NGCCCGGAAA ATAAACTTGG NGGGGGGGNA AAACCT